

10/509773

DT04 Rec'd PCT/PTO 28 SEP 2004

WO 03/083102

PCT/CA03/00393

SEQUENCE LISTING

<110> Delaney, Allen

<120> Cancer Associated Protein Phosphatases and their  
uses

<130> KINE-040PRV

<140> unknown

<141>

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (0)...(0)

<223> MKPX polynucleotide

<400> 1

ggcacgaggc cgagccctgt gcctcccacg cccggcgccc gcgagccggg gtccgcgagg	60
gccccgggtggg gcgccggcagc cagaaccgg actacgaatc ccaggggtcg ggcggggcgga	120
gccccgggggg acgctggggcc tgcggcgtgc gcacgggggc ggggaccggc aaggcgggac	180
catttccccgg cataggotcc ggtgccccctg cccggctccc gccgggaagt tctaggccgc	240
cgcacagaaa gcccgtccct ccacgcccggg tctctggagc gcccctgggtt gccccggccgg	300
tccctgcggc tgacttggtg acactgcgag cactcagtcc ctcccgcccg ctcctccccc	360
gccccggcccg ccgctctcc tcctgtaaatc atgcctaatg ggcgcctgcga ccacacggcc	420
ggggcgttag cgttgcgttt cagccaccat ggggaatggg atgaacaaga tccctggccgg	480
cctgtacatc ggcacacttca aagatgccag agacgcggaa caatttgcgca agaacaaggt	540
gacacatatt ctgtctgtcc atgatagtgc caggcctatg ttggaggggag taaaatacct	600
gtgcattcca gcagcggatt caccatctca aaacctgcaca agacatttca aagaaaagtat	660
taaatttattt caccatctca ggctccgggg tgagagctgc cttgtacact gcctggccgg	720
ggtctccagg agcgtgacac tggtgatgc atacatcatg accgtactg actttggctg	780
ggaggatggcc ctgcacacccg tgccgtctgg gagatctgt gccaacccca acgtggctt	840
ccagagacag ctccaggagt ttgagaagca tgaggccat cagtatcgcc agtggctgaa	900
ggaagaatatt ggagagagcc ctttgcggg tgccagaagaa gccaaaaaca ttctggccgc	960
tccaggattt ctgaagtttcc gggcccttot cagaagactg taatgtacct gaagtttctg	1020
aaatatttgc aacccacaga gttttagctg gtgtgcggaa aaagaaaagc aacatagagt	1080
ttaagtatcc agtagtgatt tgtaaacttg tttttcattt gaagctgaat atatacgtag	1140
tcatgttat gttgagaact aaggatattc tttagcaaga gaaaatattt tccctttatc	1200
cccaactgtg tggaggtttc tgtaacctgc ttggatgc gtaaggatcc cgggagccctt	1260
gccgcactgc ctgtgggtt gcttggcgct cgtgattgct tcctgtgaac gcctcccaag	1320
gacgagccca gtgtagttgt gtggcgtaa ctctggccgt gtgttctcaa attccccagc	1380
ttggggaaaata gcccctgggtg tgggtttat ctctggtttgc ttctcccggt ggtggaaattt	1440
accgaaaagct ctatgttttc gttataataag ggcaacttag ccaagttaa aaaaaaaaaaa	1500
aaaaaaaaaaaa aaaaaaaaaaaa	1520

<210> 2

<211> 184

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (0)...(0)  
 <223> MKPX polypeptide

<400> 2  
 Met Gly Asn Gly Met Asn Lys Ile Leu Pro Gly Leu Tyr Ile Gly Asn  
 1 5 10 15  
 Phe Lys Asp Ala Arg Asp Ala Glu Gln Leu Ser Lys Asn Lys Val Thr  
 20 25 30  
 His Ile Leu Ser Val His Asp Ser Ala Arg Pro Met Leu Glu Gly Val  
 35 40 45  
 Lys Tyr Leu Cys Ile Pro Ala Ala Asp Ser Pro Ser Gln Asn Leu Thr  
 50 55 60  
 Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Arg  
 65 70 75 80  
 Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val  
 85 90 95  
 Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu  
 100 105 110  
 Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn  
 115 120 125  
 Val Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His  
 130 135 140  
 Gln Tyr Arg Gln Trp Leu Lys Glu Glu Tyr Gly Glu Ser Pro Leu Gln  
 145 150 155 160  
 Asp Ala Glu Glu Ala Lys Asn Ile Leu Ala Ala Pro Gly Ile Leu Lys  
 165 170 175  
 Phe Trp Ala Phe Leu Arg Arg Leu  
 180

<210> 3  
 <211> 2916  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> PTP4A1 polynucleotide

<400> 3  
 aaggccgcct cggcgcgtgt attggctct tgggtcgccc gccggctcgc ctacgcgctc 60  
 tgctccgagc cgctcaactgc atggtagagt ctggtgcccc cgccgcggcc tgcatcgccg 120  
 ccaccgcgc tcgcacacga ccaccgcgc ctcctgtcc tgcagccaco gccaccgcct 180  
 gtgtccgcgc cgctcgggac cggctgtatg attagccac aatcttcaat gagtaaacat 240  
 attcctaatt tctgtggtgt tcttggtcac acatttatgg agtttctgaa gggcagtgg 300  
 gattactgcc aggcacagca cgacctctat gcagacaatg gaactgtaga aactgattac 360  
 tgctccacca agaagccccataaagatgg ttatcttggaa cacagaatgt ttgaaatcca 420  
 cagacattt tacaagatgtt ctgaccttggaa tgggtaaac ctcagtcac ttctttctg 480  
 ttggcctcag tattacttggaa ttgaagaatt gctgcttctt gttagggatgt tcatttcaact 540  
 tatcattact tacaacttca tactcaaagc actgagaatt tcaagtggag tatattgaag 600  
 tagacttcag tttctttggaa tcatttctgtt attcaattttt ttaatttattt tcataaccct 660

attgagtgtt ttttaactaa attaacatgg ctcgaatgaa ccgcccagct cctgtggaaag 720  
 tcacatacaa gaacatgaga tttcttatta cacacaatcc aaccaatgcg accttaaaca 780  
 aatttataga ggaacttaag aagtatggag ttaccacaat agtaagagta tgtgaagcaa 840  
 cttatgacac tactcttgcg gagaaagaag gtatccatgt tcttattgg ccttttgatg 900  
 atgggtcacc accatccaac cagattgtt atgactgtt aagtcttgcg aaaattaagt 960  
 ttctgtgaaga acctgggtgt tttattgtt ttcattgcgt tgccaggcctt gggagagctc 1020  
 cagtaacttgt tgcccttagca ttaattgaag gtggaatgaa atacaagat gcagtaaat 1080  
 tcataagaca aaagccgcgt ggagcttta acagcaagca acttctgtat ttggagaagt 1140  
 atcgccctaa aatggccgt cggttcaaaag attccaaacgg tcatagaaac aactgttgc 1200  
 ttcaataaaaa ttgggggtgcc taatgtact ggaagtggaa cttgagatag ggcctaattt 1260  
 gttatacata ttagccaaca ttttgcgtt gtaagtctaa tgaagcttcc ataggagtat 1320  
 tggaaaggcag ttttaccagg cctcaagcta gacagattt gcaacctctg tatttgggtt 1380  
 acagtcaacc tatttggata ctggcaaaa gattcttgcgt gtcagcatat aaaatgtgct 1440  
 ttttttttttgcgtt atcaatttgc ttttttttttcaatttgcgtt atcatgcgtt attgagttt gacttgcgtt 1500  
 atctattcccc atgcceagaat ttatcaata cataagaat tttaggaagat taggtgc 1560  
 aatacccccaca acaatacttg tatatttttta gtaccatata gaagaaaaat ccaggaaact 1620  
 atgaacacta gacccatgtt gtttttttttcc ttcaagtcc tcaaaacattt aagtagggc 1680  
 ctacatggttt atttggctgc tcaattttatgt ttttttttcc ttttttttacc aagtttttaca gtgattttt 1740  
 gtcagggttgcgtt gttaccattt gtttttttttcc ttttttttacc aagtttttaca gtgattttt 1800  
 tacgtgtttt catgtatctc acctttgtt gtttttttttcc ttttttttacc aacccatccatt ttggaaatct 1860  
 acgttgttaca gaagccatgt ttttttttttcc ttttttttacc aacccatccatt ttggaaatct 1920  
 atgtttgcac ttttttttttcc ttttttttacc aacccatccatt ttggaaatct 1980  
 tatttttttttcc ttttttttacc aacccatccatt ttggaaatct 2040  
 ttaattttttcc ttttttttacc aacccatccatt ttggaaatct 2100  
 ttttttttttcc ttttttttacc aacccatccatt ttggaaatct 2160  
 ttgttttttttcc ttttttttacc aacccatccatt ttggaaatct 2220  
 ttttttttttcc ttttttttacc aacccatccatt ttggaaatct 2280  
 ttaatatttttcc ttttttttacc aacccatccatt ttggaaatct 2340  
 ttaatgttag ttcaaccata ttttttttcc ttttttttacc aacccatccatt ttggaaatct 2400  
 gagaataat ttttttttcc ttttttttacc aacccatccatt ttggaaatct 2460  
 ctaaataaat aatgcacatgc ttttttttcc ttttttttacc aacccatccatt ttggaaatct 2520  
 ttttttttttcc ttttttttacc aacccatccatt ttggaaatct 2580  
 taaatgttagg attataaatg atgtcagcat ttttttttcc ttttttttacc aacccatccatt ttggaaatct 2640  
 ggttccatcat gaaaacttta atactaaaag cactttccat ttttttttcc ttttttttacc aacccatccatt ttggaaatct 2700  
 agataattttt gaaaccatattt attatttttttcc ttttttttacc aacccatccatt ttggaaatct 2760  
 agcccttgggtt ttttttttcc ttttttttacc aacccatccatt ttggaaatct 2820  
 agtttttttcc ttttttttacc aacccatccatt ttggaaatct 2880  
 atatttttttcc ttttttttacc aacccatccatt ttggaaatct 2916

<210> 4  
 <211> 173  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (0)...(0)  
 <223> PTP4A1 polypeptide sequence

<400> 4  
 Met ala Arg Met Asn Arg Pro Ala Pro Val Glu Val Thr Tyr Lys Asn  
 1 5 10 15  
 Met Arg Phe Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys  
 20 25 30  
 Phe Ile Glu Glu Leu Lys Lys Tyr Gly Val Thr Thr Ile Val Arg Val  
 35 40 45

Cys Glu Ala Thr Tyr Asp Thr Thr Leu Val Glu Lys Glu Gly Ile His  
 50 55 60  
 Val Leu Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Ser Asn Gln Ile  
 65 70 75 80  
 Val Asp Asp Trp Leu Ser Leu Val Lys Ile Lys Phe Arg Glu Glu Pro  
 85 90 95  
 Gly Cys Cys Ile Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro  
 100 105 110  
 Val Leu Val Ala Leu Ala Leu Ile Glu Gly Gly Met Lys Tyr Glu Asp  
 115 120 125  
 Ala Val Gln Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys  
 130 135 140  
 Gln Leu Leu Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe  
 145 150 155 160  
 Lys Asp Ser Asn Gly His Arg Asn Asn Cys Cys Ile Gln  
 165 170

<210> 5  
 <211> 2759  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> PTPN7 polynucleotide sequence

<400> 5  
 ggcacgagggc aagaggcagc ctggggggcca cagctgcttc agcagaccc tc atggctgagt 60  
 gagcctcccc tggggccccc acccccaccc tc agcatggtcc aagccatggg gggcgctcca 120  
 gaggcacaggg cttgacccttgc tctttggggg cagccatgac ccagctccg cctgaaaaaaaa 180  
 cgccagccaa gaagcatgtg cgactgcagg agaggcgaaaa ctccaatgtg gctctgtatgc 240  
 tggacgttcg gtccctgggg gccgttagaac ccatactgtc tgtgaacaca ccccgaaaagg 300  
 tcaccctaca ctttctgcgc actgctggac acccccttac ccgctggggcc .cttcagcgcc 360  
 agccacccag ccccaagcaa ctggaaagaag aattcttggaa gatcccttca aactttgtca 420  
 gccccgaaga cctggacatc cctggccacg cctccaaaggcc cccgatatacg accatcttgc 480  
 caaatcccca gagccgtgtc tgtctaggcc gggcacagag ccaggaggac ggagattaca 540  
 tcaatgccaa ctacatccga ggctatgacg ggaaggagaa ggtctacatt gccacccagg 600  
 gccccatgcc caacactgtg tggacttct gggagatgtt gtggcaagag gaagtgtccc 660  
 tcattgtcat gctcaactcg cttcgagagg gcaaggagaa atgtgtccac tactggggcca 720  
 cagaagagga aacctatggc cccttccaga tccgcatcca ggacatgaaa gagtggcccg 780  
 aatacactgt gccggcacgtc accatccagt accaggaaga gcgcgggtca gtaaaggcaca 840  
 tcctcttttc ggcctggcca gaccatcaga caccagaatc agctggggcc ctgctgcgcc 900  
 tagtggcaga ggtggaggag agccccggaga cagccggccca ccccgccct atctgttgtcc 960  
 actgcagtgc agggattggc cggacgggtc gtttcatcgcc cacggcaatt ggctgtcaac 1020  
 agctgaaagc cccgaggagaa gtggacattc tgggtattgt gtgcctactg cggcttagaca 1080  
 gaggggggat gatccagacg gcagagcgtt accaggatcc tcaaccactt ttggccctgt 1140  
 atgcaggcca gctgcttgag gaacccagcc cctgaccctt gccaccctcc ggtggcccg 1200  
 gtgcctactt ccctcaagcc tggttgggtt ggttggggaa aagtggccg agtgtatctgg 1260  
 gggtacccctt ggggttgggtt gggggaggag tgcccttca gtgggtctt acagtcacag 1320  
 gaagcagcag cagtaaggac aaggggccgg attcaggatcc tcaaccactg gccactccctc 1380  
 ttgccttctt ctgttggggcc cagatggaca gtaaggggaa cctccaaatgt ctctctgaac 1440  
 ttaaagacag gagctggcat ttatgacaga caaagaaga agccccagggtg tcctgggttt 1500  
 ctctgagaca ctctttgttga tcttcagttt cctgttctat aacatgaaca taagtgttta 1560  
 gctgccatga gggaaaagta atgagagaag ttctagaagc cactccagcc actcccttctt 1620  
 ggggctgaca aaagggttatca tccttcaccc gagttctgc ccaagcacag 1680

gccagatgca agaatgggaa aaagtctggt cctgatctcc aagtctcaac atccttatcag 1740  
 tgactctgcc tccctgacca cacatcgaa gggcctggat gacccaatca aaagaaaagaa 1800  
 caaggactct ggtaaccctt gcctccaccc atgtgtcata agagtaggct acagaggtga 1860  
 ccaggcctgg cagttaaaat ctctggaaga gggAACATGT ggggactact cagaggcaaa 1920  
 gaggagctgc tcctgcctcc atgggtgctg gccactccca ccaactactc tttagggaggc 1980  
 taaggactct ctgtttgac cttccatggc tcaataatac ctggatgcag gaccactata 2040  
 ccttcattt gctgagtgaca ccttagagagc ttggctgtt caaaaaacaa tcagggtcat 2100  
 aaccatccat gcagacatgg aggctcggt gaaccaggac tccteactgt ctacctgaga 2160  
 gaatgagcac ccctcatcca ttcagcatc aacacattt ccaggggacc tcaggtctac 2220  
 ctcaggactg aaccggccaca cctcaggatt ctccttcctt gaatctgaga ctggctgccc 2280  
 attctgagat ggggatgaag gtaagatgcc gcatcaccag cacggcccc ctgacagctg 2340  
 ccttgatacc agctctctgt gaaaaccccc gaggagtgg atctggagaa cagctggcc 2400  
 tcctcactca ggactctct cctgaagaac acgcagtgtc aaaactgagg atgatttccc 2460  
 taatgcttct gcttgagtc tcttatggag gagctgtcc ttcccttacag cttggggatg 2520  
 gacttccac acctccacct cccctgagcc ctgagccctg tgagaggacg actgtctatg 2580  
 caatgaggtc cggtgggggg ctctcaagtg cctgatctg cctggctcag aggccagccag 2640  
 agggaaagcaa ctgacagccc cacaggccct ccctggcact gtccccatct cagagctcag 2700  
 gagggtacaa gctccagaac agtaaccaag tggaaaata aagacttctt ggatgactg 2759

<210> 6  
 <211> 339  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (0)...(0)  
 <223> PTPN7 polypeptide sequence

<400> 6  
 Met Thr Gln Pro Pro Pro Glu Lys Thr Pro Ala Lys Lys His Val Arg  
 1 5 10 15  
 Leu Gln Glu Arg Arg Gly Ser Asn Val Ala Leu Met Leu Asp Val Arg  
 20 25 30  
 Ser Leu Gly Ala Val Glu Pro Ile Cys Ser Val Asn Thr Pro Arg Glu  
 35 40 45  
 Val Thr Leu His Phe Leu Arg Thr Ala Gly His Pro Leu Thr Arg Trp  
 50 55 60  
 Ala Leu Gln Arg Gln Pro Pro Ser Pro Lys Gln Leu Glu Glu Phe  
 65 70 75 80  
 Leu Lys Ile Pro Ser Asn Phe Val Ser Pro Glu Asp Leu Asp Ile Pro  
 85 90 95  
 Gly His Ala Ser Lys Asp Arg Tyr Lys Thr Ile Leu Pro Asn Pro Gln  
 100 105 110  
 Ser Arg Val Cys Leu Gly Arg Ala Gln Ser Gln Glu Asp Gly Asp Tyr  
 115 120 125  
 Ile Asn Ala Asn Tyr Ile Arg Gly Tyr Asp Gly Lys Val Tyr  
 130 135 140  
 Ile Ala Thr Gln Gly Pro Met Pro Asn Thr Val Ser Asp Phe Trp Glu  
 145 150 155 160  
 Met Val Trp Gln Glu Glu Val Ser Leu Ile Val Met Leu Thr Gln Leu  
 165 170 175  
 Arg Glu Gly Lys Glu Lys Cys Val His Tyr Trp Pro Thr Glu Glu Glu  
 180 185 190  
 Thr Tyr Gly Pro Phe Gln Ile Arg Ile Gln Asp Met Lys Glu Cys Pro  
 195 200 205

Glu Tyr Thr Val Arg His Val Thr Ile Gln Tyr Gln Glu Glu Arg Arg  
 210 215 220  
 Ser Val Lys His Ile Leu Phe Ser Ala Trp Pro Asp His Gln Thr Pro  
 225 230 235 240  
 Glu Ser Ala Gly Pro Leu Leu Arg Leu Val Ala Glu Val Glu Glu Ser  
 245 250 255  
 Pro Glu Thr Ala Ala His Pro Gly Pro Ile Val Val His Cys Ser Ala  
 260 265 270  
 Gly Ile Gly Arg Thr Gly Cys Phe Ile Ala Thr Arg Ile Gly Cys Gln  
 275 280 285  
 Gln Leu Lys Ala Arg Gly Glu Val Asp Ile Leu Gly Ile Val Cys Gln  
 290 295 300  
 Leu Arg Leu Asp Arg Gly Gly Met Ile Gln Thr Ala Glu Gln Tyr Gln  
 305 310 315 320  
 Phe Leu His His Thr Leu Ala Leu Tyr Ala Gly Gln Leu Pro Glu Glu  
 325 330 335  
 Pro Ser Pro

<210> 7  
 <211> 3960  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> FEM-2 polynucleotide

<400> 7  
 ggacacggag ccgcgaggag acagctgagg cccgcggaga ccaggggggt aagcctggag 60  
 acccttgc cctggcttag ctgcaggccc cgggatgct ttgggcattgt cctctggagc 120  
 cccacagaag agcagccaa tggccagtgg agctgaggag accccaggct tcctggacac 180  
 gtcctgcaa gacttcccaag ccctgctgaa cccagaggac cctctgcccatt ggaaggcccc 240  
 agggacggtg ctcagccagg aggaggtgg aggcggagctg gctgagctgg ccatgggctt 300  
 tctggcagc aggaaggccc cgccaccact tgctgctgct ctggcccacg aagcaggttc 360  
 acagctgcta cagacagacc tttccgaatt caggaagttt cccagggagg aagaagaaga 420  
 ggaggaggac gatgacgagg aggaaaaggc ccctgtgacc ttgctggatg cccaaaggct 480  
 ggcacagagt ttcttaacc gcctttggga agtgcggcgc cagtggcaga agcaggtgcc 540  
 attggctgcc cgggcctcac agcggeactg gctggcttcc atccacgcca tccggaaacac 600  
 tcgcccgaag atggaggaccc ggcacgtgtc cctcccttcc ttcaaccagc tctteggctt 660  
 gtctgaccct gtgaaccgcg cctacttgc tggatgttgc ggtcacggag gctgtggatgc 720  
 tgcgaggtac gccgtgtcc acgtgcacac caacgctgcc cgccagccag agctgcccac 780  
 agaccctgag ggacccctca gagaaggctt cggcgcacc gaccagatgt ttctcaggaa 840  
 agccaagcga gagcggcgtgc agagcggcac cacagggtgtc tgtgcgtca ttgcaggagc 900  
 gaccctgcac gtgccttgc tcgggattc ccaggcttcc ttgttacagc agggacagg 960  
 ggtgaagctg atggagccac acagaccaga acggcaggat gagaaggcgc gcattgaagc 1020  
 attgggtggc ttgtgtctc acatggactg ctggagatc aacggjaccg tggccgtctc 1080  
 cagagccatc ggggatgttot tccagaagcc ctacgtgtct ggggaggccg atgcagcttc 1140  
 ccggggctg acgggctccg aggactacct gctgtttgc tggatgttgc tctttgacgt 1200  
 cgtacccac caggaagttt ttggccgtt ccagagccac ctgaccaggc agcaggccag 1260  
 cgggctccgt gtgcggcggagg agctgggtgc tgccggccgg gagcggggct cccacgacaa 1320  
 catcacggtc atgggtgtct tccctcaggaa ccccaagag ctgctggagg gcggaaacca 1380  
 gggagaaggg gaccccccagg cagaaggagg gagcaggac ttgccttcca gccttccaga 1440  
 acctgagacc caggctccac caagaagcta ggtgtttcc agggccctgc cctcccttc 1500  
 etccccatctt tgccttctc tccctcaggaa gcctcaggac ccaacaggtg gcaggcagt 1560

gacagggtgc ccgccccaca gtgctttccc cagcacccca gagccagtgc ggacacccccc 1620  
 cgcagcccggt cctgggtggc gtggaactgc actgggtggc gggcagatgg tggaaaggcag 1680  
 cttaggagac ctcaccaaag agaagatggc cggctcttgc ctccccagtc ctattaggcc 1740  
 cgggggtggga ccagaggtca taggtgccc acggcagccaa aaccaaagac actgggtgtc 1800  
 atggggcagc atgggtgtc acgtgggacc ctggggcggg cccaggagcc aaactcttgc 1860  
 agcacccctt gggcaggcc cagcagcggg gtggccagcc ccagttccc attgtcttc 1920  
 tctgcccgc gggccagggt gttcatatt tacagatatg cccagccagt cctggtcggc 1980  
 cacaccagtgc tcccaaagag gagagcgcag cagagccagg ggtctgttgc gtacgcggca 2040  
 ccccccctggc cccactcccg ggcagccatg atgtgttgc cccaccaggc cttccgggc 2100  
 tgctctcttc cctgagcccg gaaccggcga cgcacatgtc tttttgttg gtgtgttgt 2160  
 tttttccag ggaggctaa ttccgaagca gtattccagg ttttctctt ttttatcag 2220  
 tgccaagatg acctgttgc tcataattta taagcagac ttagcattta ttttattctt 2280  
 tagaaaaactt aagtatttac ttttttaaag ctattttca aggaaccttt ttttgcagta 2340  
 ttattgaatt tatttctaa atcaggattg aaacaggaac ttttccagggt ggtgttaata 2400  
 agccattcaa gtgccttaca cagctttgaa gaaactagga ctgcagtgcc ctcggatagg 2460  
 cccatttggg tttttagaaa agcaggattt gttttgttag ggaggcatga ttttggtgag 2520  
 atctttctgg aagaggtttc cgcctctttg tgatgtgaa caccccaag gtttccccc 2580  
 ccccccgcgtc cccaggtgc tggcaggagc tgcgcactgc acgttagtgg gcctggggcc 2640  
 gacagcgggg ctctggcat cccgggtgac cttggccat ctgcctgcatttccacccccc 2700  
 ttggggcctgg ctggatccca ggcagaggga ctttgcgtgt gtgtgttgg aacattttca 2760  
 aatatctttt gaatttgtaa tcaaatttggt ctcatggaa aagactctta attaagaggc 2820  
 tcaggcaagc acagaggcag cccgtgggtc tctgtctcag tctggaggca gcagggtatgc 2880  
 tgctggaggt ccatggcaca ggcacacggc ctcacatggc cgcgggtggc tggcagcacg 2940  
 cctgccttgc tctgccttgc gcccctgaaca ggcacatggc ctccacgttcc cctagtgcac 3000  
 cctgagagggg ggctcacaag tgaccgatcc tgggtgcctc agggagctca ctgagggcgt 3060  
 gcaaaaggta aagtggcaag gctgggggag ggtgtcggtt agagggaaaga gggcagggggg 3120  
 ctaggggagg actcagaggc catctgcagg gccaagccac aggaagggtc gagctggagg 3180  
 tgggcaggggc tgctccaggc agtgcaggagc agtgcagggg gaggagagga gaaaggagg 3240  
 aagctgggtc gtgtgtccc catgaaggca ttcaagatcc acctgcacac agcggagagcc 3300  
 ccaggaaggt ttgcacagct gtgccttcaag caccctggcc tctctcagc tcgcccggag 3360  
 ggcacgctag agccgccttc cccgtggggag ccctctgtcc cacaggggc ggggagccag 3420  
 ctttgcgtggg gcccctacctg catgcccagc cttacccttc attctcacag cacagatgag 3480  
 gttgagacca tgcaaatgcattgtcta aggtcttta tttacaaaaaaa aaaaccttaa 3540  
 acatagtgc tgtcattcag acattcagag aatgggtggc cacaacaaat gaccaagtat 3600  
 tgcttggctt aacttgaagg cctgtctgtc ctttctgggg gtcaggagc cagctccacc 3660  
 ctcaccacta gcccacccctg cccgtggggca taaccttgc acagagagag aatgattggc 3720  
 atctgcattt ctctttttt tctaataat tctgttctgt gctggcggaga gtgaagtttc 3780  
 accatgtgga ggtttggcctt ctatcacctg gtggtctgtat tcataccctt gctgaggct 3840  
 ccactggaaag atctcgccagc ctcagttgtat gggaaacctt ttccccaggc ttgtcccaggc 3900  
 actgcccgtc cccacccctg agccaggacc ccagaggatg gccatggccc gtgcctggca 3960

<210> 8  
 <211> 454  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (0)...(0)  
 <223> FEM-2 polypeptide sequence

<400> 8  
 Met Ser Ser Gly Ala Pro Gln Lys Ser Ser Pro Met ala Ser Gly Ala  
 1 5 10 15  
 Glu Glu Thr Pro Gly Phe Leu Asp Thr Leu Leu Gln Asp Phe Pro Ala  
 20 25 30

Leu Leu Asn Pro Glu Asp Pro Leu Pro Trp Lys Ala Pro Gly Thr Val  
     35                        40                        45  
 Leu Ser Gln Glu Glu Val Glu Gly Glu Leu Ala Glu Leu Ala Met Gly  
     50                        55                        60  
 Phe Leu Gly Ser Arg Lys Ala Pro Pro Pro Leu Ala Ala Ala Leu Ala  
     65                        70                        75                        80  
 His Glu Ala Val Ser Gln Leu Leu Gln Thr Asp Leu Ser Glu Phe Arg  
     85                        90                        95  
 Lys Leu Pro Arg Glu Glu Glu Glu Glu Asp Asp Asp Glu Glu-  
     100                       105                       110  
 Glu Lys Ala Pro Val Thr Leu Leu Asp Ala Gln Ser Leu Ala Gln Ser  
     115                       120                       125  
 Phe Phe Asn Arg Leu Trp Glu Val Ala Gly Gln Trp Gln Lys Gln Val  
     130                       135                       140  
 Pro Leu Ala Ala Arg Ala Ser Gln Arg Gln Trp Leu Val Ser Ile His  
     145                       150                       155                       160  
 Ala Ile Arg Asn Thr Arg Arg Lys Met Glu Asp Arg His Val Ser Leu  
     165                       170                       175  
 Pro Ser Phe Asn Gln Leu Phe Gly Leu Ser Asp Pro Val Asn Arg Ala  
     180                       185                       190  
 Tyr Phe Ala Val Phe Asp Gly His Gly Gly Val Asp Ala Ala Arg Tyr  
     195                       200                       205  
 Ala Ala Val His Val His Thr Asn Ala Ala Arg Gln Pro Glu Leu Pro  
     210                       215                       220  
 Thr Asp Pro Glu Gly Ala Leu Arg Glu Ala Phe Arg Arg Thr Asp Gln  
     225                       230                       235                       240  
 Met Phe Leu Arg Lys Ala Lys Arg Glu Arg Leu Gln Ser Gly Thr Thr  
     245                       250                       255  
 Gly Val Cys Ala Leu Ile Ala Gly Ala Thr Leu His Val Ala Trp Leu  
     260                       265                       270  
 Gly Asp Ser Gln Val Ile Leu Val Gln Gln Gly Gln Val Val Lys Leu  
     275                       280                       285  
 Met Glu Pro His Arg Pro Glu Arg Gln Asp Glu Lys Ala Arg Ile Glu  
     290                       295                       300  
 Ala Leu Gly Gly Phe Val Ser His Met Asp Cys Trp Arg Val Asn Gly  
     305                       310                       315                       320  
 Thr Leu Ala Val Ser Arg Ala Ile Gly Asp Val Phe Gln Lys Pro Tyr  
     325                       330                       335  
 Val Ser Gly Glu Ala Asp Ala Ala Ser Arg Ala Leu Thr Gly Ser Glu  
     340                       345                       350  
 Asp Tyr Leu Leu Ala Cys Asp Gly Phe Phe Asp Val Val Pro His  
     355                       360                       365  
 Gln Glu Val Val Gly Leu Val Gln Ser His Leu Thr Arg Gln Gln Gly  
     370                       375                       380  
 Ser Gly Leu Arg Val Ala Glu Glu Leu Val Ala Ala Ala Arg Glu Arg  
     385                       390                       395                       400  
 Gly Ser His Asp Asn Ile Thr Val Met Val Val Phe Leu Arg Asp Pro  
     405                       410                       415  
 Gln Glu Leu Leu Glu Gly Gly Asn Gln Gly Glu Gly Asp Pro Gln Ala  
     420                       425                       430  
 Glu Gly Arg Arg Gln Asp Leu Pro Ser Ser Leu Pro Glu Pro Glu Thr  
     435                       440                       445  
 Gln Ala Pro Pro Arg Ser  
     450

<211> 2786  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (0)...(0)  
<223> DKFZP566K0524 polynucleotide

<400> 9

tggacccaac tggcgaggct gctgggggtt cagcgggaca gttggggccgg ccccgccaggc 60  
ccaggtttt gaaaataaaag ttaattcaga gaaggtaaaa ctcttccttc gaaatttccc 120  
acataatgtat tatgaggatg ttttgaaga gccttcagaa agtgcagtgc atccccagcat 180  
gtggacagcc agaggccctc tcagaagaga caggtggagc agtgaggatg aggaggctgc 240  
agggccatca caggctctct ccctctact ttctgatacg cgcaaaattt tttctgaagg 300  
agaactagat cagttggctc agattccggcc attaatatttc aattttcatg agcagacagc 360  
catcaaggat tgtttggaaa tcccttggagaaaaaacacgc gctgtatgata tcatgcggg 420  
atttatggct ttagaactta agaatctgcc tggtgaggatc tactctggga atcaaccaag 480  
caacagagaa aaaaacagat accggatatact tcttccatattt gattcaacac gcgttccctct 540  
tggaaaaggc aaggactaca tcaatgctat ttatattttaga atatgtcaattt gtggagaaga 600  
gtatttttt atcgctactc aaggaccact gctgagcacc atatgtactt tttggcaat 660  
ggtgttggaa aataattcaa atgttattgc catgataacc agagagatgg aaggtggat 720  
tatcaaattgc taccattact ggcccatattc tctgaagaag ccatttggaaat tggaaacactt 780  
ccgtgtatttc ctggagaactt accagataact tcaatatttc atcatttgc ttttcaagt 840  
tggggagaag tccacgggaa ctatgtactc tgtaaaacag ttgcagttca ccaagtggcc 900  
agaccatggc actcttcgcct cagcagatag cttcataaaaa tatatttcgtt atgcaaggaa 960  
gagccaccc acaggaccca tgggtgttca ctgcagtgc ggcataaggcc ggacaggggt 1020  
gttccatgtgtt gttgtatgtcg ttttctgtgc catcgtaaag gactgttcat tcaacatcat 1080  
ggatatagtg gcccaaatatg gagaacaacg ttctggcatg gttcaaaacga aggagcagta 1140  
tcacttttttgc ttcgtatattt tgcttgaagt ttttggaaa ctctgactt tggattaaga 1200  
aagacttcgtt ttcgttctca ctttggaaat tcaatgttgc ttttccatcc ttttccatcc 1260  
catgttttgc ttcgttgc ttttggaaat tcaatgttgc ttttccatcc ttttccatcc 1320  
gtttattttc ttttggaaat ttcgttgc ttttggaaat tcaatgttgc ttttccatcc 1380  
gtttacttat ttttggaaat ttcgttgc ttttggaaat tcaatgttgc ttttccatcc 1440  
agatgttaca taaaacgtt gcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 1500  
aaaggattta aaatataatttca ttttggaaat tcaatgttgc ttttccatcc 1560  
gatttccagg actttgttgc ttttggaaat tcaatgttgc ttttccatcc 1620  
cttccaggca ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 1680  
tgctggcatt ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 1740  
acaaaatttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 1800  
agacctgttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 1860  
aaaactaaaaat ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 1920  
cttccatcc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 1980  
ttacccatcc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2040  
cattattata taatttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2100  
taagatctt ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2160  
ctcaccttc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2220  
tcatagtc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2280  
cagtaattttt ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2340  
ttctgggtgc aagctatacc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2400  
agtttaactc aatggagatc agaatatttc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2460  
ataaaatctt ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2520  
ttgggttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2580  
tgtttaaatca aatagatgtat ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2640  
ttcatttttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2700  
gtaaaataat ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2760  
aataaaaat ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttggaaat tcaatgttgc ttttccatcc 2786

<210> 10  
<211> 398  
<212> PRT  
<213> Homo sapiens

<220>  
<221> UNSURE  
<222> (0)...(0)  
<223> DKFZP566K0524 polypeptide

<400> 10  
Gly Pro Asn Trp Arg Gly Cys Trp Gly Cys Ser Gly Thr Val Gly Ala  
1 5 10 15  
Ala Pro Gln Ala Gln Val Phe Glu Asn Lys Val Asn Ser Glu Lys Val  
20 25 30  
Lys Leu Ser Leu Arg Asn Phe Pro His Asn Asp Tyr Glu Asp Val Phe  
35 40 45  
Glu Glu Pro Ser Glu Ser Gly Ser Asp Pro Ser Met Trp Thr Ala Arg  
50 55 60  
Gly Pro Phe Arg Arg Asp Arg Trp Ser Ser Glu Asp Glu Glu Ala Ala  
65 70 75 80  
Gly Pro Ser Gln Ala Leu Ser Pro Leu Leu Ser Asp Thr Arg Lys Ile  
85 90 95  
Val Ser Glu Gly Glu Leu Asp Gln Leu Ala Gln Ile Arg Pro Leu Ile  
100 105 110  
Phe Asn Phe His Glu Gln Thr Ala Ile Lys Asp Cys Leu Lys Ile Leu  
115 120 125  
Glu Glu Lys Thr Ala Ala Tyr Asp Ile Met Gln Glu Phe Met Ala Leu  
130 135 140  
Glu Leu Lys Asn Leu Pro Gly Glu Phe Tyr Ser Gly Asn Gln Pro Ser  
145 150 155 160  
Asn Arg Glu Lys Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr  
165 170 175  
Arg Val Pro Leu Gly Lys Ser Lys Asp Tyr Ile Asn Ala Ser Tyr Ile  
180 185 190  
Arg Ile Val Asn Cys Gly Glu Tyr Phe Tyr Ile Ala Thr Gln Gly  
195 200 205  
Pro Leu Leu Ser Thr Ile Asp Asp Phe Trp Gln Met Val Leu Glu Asn  
210 215 220  
Asn Ser Asn Val Ile Ala Met Ile Thr Arg Glu Met Glu Gly Ile  
225 230 235 240  
Ile Lys Cys Tyr His Tyr Trp Pro Ile Ser Leu Lys Lys Pro Leu Glu  
245 250 255  
Leu Lys His Phe Arg Val Phe Leu Glu Asn Tyr Gln Ile Leu Gln Tyr  
260 265 270  
Phe Ile Ile Arg Met Phe Gln Val Val Glu Lys Ser Thr Gly Thr Ser  
275 280 285  
His Ser Val Lys Gln Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr  
290 295 300  
Pro Ala Ser Ala Asp Ser Phe Ile Lys Tyr Ile Arg Tyr Ala Arg Lys  
305 310 315 320  
Ser His Leu Thr Gly Pro Met Val Val His Cys Ser Ala Gly Ile Gly  
325 330 335  
Arg Thr Gly Val Phe Leu Cys Val Asp Val Val Phe Cys Ala Ile Val  
340 345 350  
Lys Asp Cys Ser Phe Asn Ile Met Asp Ile Val Ala Gln Met Arg Glu  
355 360 365

Gln	Arg	Ser	Gly	Met	Val	Gln	Thr	Lys	Glu	Gln	Tyr	His	Phe	Cys	Tyr
370						375					380				
Asp	Ile	Val	Leu	Glu	Val	Leu	Arg	Lys	Leu	Leu	Thr	Leu	Asp		
385						390					395				

<210> 11  
<211> 2226  
<212> DNA  
<213> Homo sapiens

```
<220>
<221> misc_feature
<222> (0)...(0)
<223> FLJ20313 nucleotide sequence
```

aaaagt  
<210> 12  
<211> 451

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (0)...(0)  
 <223> FLJ20313 polypeptide sequence

<400> 12  
 Met Pro Leu Gln Lys Phe His Tyr Arg Asn Leu Leu Leu Gly Glu His  
 1 5 10 15  
 Asp Val Pro Leu Thr Cys Ile Glu Gln Ile Val Thr Val Asn Asp His  
 20 25 30  
 Lys Arg Lys Gln Lys Val Leu Gly Pro Asn Gln Lys Leu Lys Phe Asn  
 35 40 45  
 Pro Thr Glu Leu Ile Ile Tyr Cys Lys Asp Phe Arg Ile Val Arg Phe  
 50 55 60  
 Arg Phe Asp Glu Ser Gly Pro Glu Ser Ala Lys Lys Val Cys Leu Ala  
 65 70 75 80  
 Ile Ala His Tyr Ser Gln Pro Thr Asp Leu Gln Leu Leu Phe Ala Phe  
 85 90 95  
 Glu Tyr Val Gly Lys Lys Tyr His Asn Ser Ala Asn Lys Ile Asn Gly  
 100 105 110  
 Ile Pro Ser Gly Asp Gly Gly Gly Gly Gly Asn Gly Ala  
 115 120 125  
 Gly Gly Ser Ser Gln Lys Thr Pro Leu Phe Glu Thr Tyr Ser Asp  
 130 135 140  
 Trp Asp Arg Glu Ile Lys Arg Thr Gly Ala Ser Gly Trp Arg Val Cys  
 145 150 155 160  
 Ser Ile Asn Glu Gly Tyr Met Ile Ser Thr Cys Leu Pro Glu Tyr Ile  
 165 170 175  
 Val Val Pro Ser Ser Leu Ala Asp Gln Asp Leu Lys Ile Phe Ser His  
 180 185 190  
 Ser Phe Val Gly Arg Arg Met Pro Leu Trp Cys Trp Ser His Ser Asn  
 195 200 205  
 Gly Ser Ala Leu Val Arg Met Ala Leu Ile Lys Asp Val Leu Gln Gln  
 210 215 220  
 Arg Lys Ile Asp Gln Arg Ile Cys Asn Ala Ile Thr Lys Ser His Pro  
 225 230 235 240  
 Gln Arg Ser Asp Val Tyr Lys Ser Asp Leu Asp Lys Thr Leu Pro Asn  
 245 250 255  
 Ile Gln Glu Val Gln Ala Ala Phe Val Lys Leu Lys Gln Leu Cys Val  
 260 265 270  
 Asn Glu Pro Phe Glu Glu Thr Glu Lys Trp Leu Ser Ser Leu Glu  
 275 280 285  
 Asn Thr Arg Trp Leu Glu Tyr Val Arg Ala Phe Leu Lys His Ser Ala  
 290 295 300  
 Glu Leu Val Tyr Met Leu Glu Ser Lys His Leu Ser Val Val Leu Gln  
 305 310 315 320  
 Glu Glu Glu Gly Arg Asp Leu Ser Cys Cys Val Ala Ser Leu Val Gln  
 325 330 335  
 Val Met Leu Asp Pro Tyr Phe Arg Thr Ile Thr Gly Phe Gln Ser Leu  
 340 345 350  
 Ile Gln Lys Glu Trp Val Met Ala Gly Tyr Gln Phe Leu Asp Arg Cys  
 355 360 365  
 Asn His Leu Lys Arg Ser Glu Lys Glu Ser Pro Leu Phe Leu Leu Phe  
 370 375 380

Leu Asp Ala Thr Trp Gln Leu Leu Glu Gln Tyr Pro Ala Ala Phe Glu  
385 390 395 400  
Phe Ser Glu Thr Tyr Leu Ala Val Leu Tyr Asp Ser Thr Arg Ile Ser  
405 410 415  
Leu Phe Gly Thr Phe Leu Phe Asn Ser Pro His Gln Arg Val Lys Gln  
420 425 430  
Ser Thr Val Ser Arg Ile Lys Ser Cys Thr Lys Gln Asp Tyr Phe Pro  
435 440 445  
Ser Arg Val  
450